

Gencore version 5.1.4-p5-4578  
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 19:54:31 ; Search time 57.092 seconds  
 (without alignments) 13439.802 Million cell updates/sec

Title: US-10-027-000-3  
 Perfect score: 2502  
 Sequence: 1 atggatgtatggatgttga.....attggatgtatggatgttga 2502

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:  
 1: /cgn2\_6/podata/1/ina5a\_COMB.seq:/\*  
 2: /cgn2\_6/podata/1/ina5b\_COMB.seq:/\*  
 3: /cgn2\_6/podata/1/ina6a\_COMB.seq:/\*  
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 5: /cgn2\_6/podata/1/ina\_PCTUS\_COMB.seq:/\*  
 6: /cgn2\_6/podata/1/ina/Backfiles1.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No. Score Query Length DB ID

Description

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23	23	78.2	3.1	1647	1	US-08-083-948-13
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27	27	78.2	3.1	1865	1	US-08-083-948-7

### ALIGNMENTS

RESULT 1  
 Sequence 11, Application US/09434288

; Patent No. 6303767  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bettach C., Melanie  
 ; APPLICANT: McDaniel, Robert

; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA

; TITLE OF INVENTION: CONSTRUCT THEREFOR  
 ; FILE REFERENCE: 30062-20030.00

; CURRENT APPLICATION NUMBER: US/09/434,288

; PRIORITY APPLICATION NUMBER: 60/107,093  
 ; PRIORITY FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 11  
 ; LENGTH: 3241

; TYPE: DNA  
 ; ORGANISM: Streptomyces narbonensis

US-09-434-288-11

Query Match 7.4%; Score 184.4; DB 4; Length: 3241;  
 Best Local Similarity 48.2%; Pred. No. 6.3e-31;  
 Matches 1028; Conservative 0; Mismatches 956; Indels 150; Gaps 12;

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EARLIER FILING DATE: 1998-05-28  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO: 20  
 LENGTH: 2401  
 TYPE: DNA  
 ORGANISM: Streptomyces venezuelae  
 us-09-320-878-20

Query Match 7.2%; Score 179; DB 3; Length 2401;  
 Best Local Similarity 47.7%; Pred. No. 8.5e-30; Mismatches 966; Indels 150; Gaps 11;  
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Qy 206 CGCTCGGTTCACATTCAACCAACTCTGCTCAAAGAGCAGGCTAATGATGATGGCAAAG 265  
 Db 255 CCCCGCCAGCAGACTTCAGACACATGGCCACACTACGGCAAGTGTGGCGCG 314  
 Qy 266 AGGCATCGCTAAAGATGTCGATGTGATGTCGCGCGACTAACATGCAAAGCCTCC 325  
 . 315 AGCGTCCGCGCTAACCGAGGATGGTCTGAGTCGATGTCGAGGATGGTCTGGAG 385  
 Qy 326 CTCGGGAGACCTGGCTAACCGAGGATGGTCTGAGTCGATGTCGAGGAGCCCTGGAG 374  
 Db 375 CGAACGGGGCGCAGACTACGAGACCTTCAGGAGAC 434  
 Qy 386 CTGGGCTCTCATCGGCCATCTAGACCACTCGAGTCAGGCTACGGTACATCAGACATT 445  
 Db 435 CGGCGCCAGATCAAGGGCATCGAGGTCAGGTGCGGTCTGATGACCGGCCAGCACCTCG 494  
 Qy 446 TGTGCAATGATCAGGAGGACAGGGCAATGATGATGGTGCAGAGCTCGTACGGAGGGCTC 505  
 Db 495 CGGCCAACACAGGAGACACCGCTTCGGCTTCGGAACGCCATGACGAGCAGAC 554  
 Qy 506 TCCGTAAATCTGGACTCCCGTCCAGATCTGTGCGAGACTCCAGGGGGCGT 565  
 Db 555 TCCGGAGATCAGGTTCGGCTTCGAG--GGCTCTCAGGGGGGGCTCT 611  
 Qy 566 TCTAGACGGTACATGCAATGCGTCAATGCGTGTGCGAGGAGACCGCCATATACTTG 625  
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 Qy 1166 ACCAGTCCCTAACGCCACATGGGCTCATGGGCTGGGCTAACAGGCC 1225  
 Db 1184 CGCGGGTGGTGGAGGTGAGCTAGAGAGGGAGCTTGGGAGCGAG 1243  
 Qy 1226 CTGGTACCCCTAACGCCACATGGGCTGAGCTTGGGAGACCTTGGGAGCGAC 1285  
 Db 1244 ATCCCGGGGAACCTCAGC-----CCGGCGTCAAC 1277  
 Qy 1286 TGGTGGACTTACACCCCAAGGGGCAACACTGGTACGGGACATGGAGGACACT 1345  
 Db 1278 AGGGCACCACCTCTGCGCCAGCGGGGGCGCTGTGACGCCACCTGACCGT 1337  
 Qy 1346 AQACCGCCAGGAGACTGCACTAGAGCTGGAGTGTGGCTCGTGTGCTGGGGCAAGG 1405  
 Db 1338 CGCCGACGSGAGTACCGATCGGGCTGACCGCTGGTGTGACGCCAC 1396  
 Qy 1406 CGTACGTTAGACGACGACTCTGTCGACACACGCCAACAGCAGTCCGGGATGCGT 1465  
 Db 1397 -----CTGGCAGCCACA 1409  
 Qy 1466 TCTTCGCTCTGCCAACGGGAGACGCGCCATCAATCTGTCAGGGCACACT 1525  
 Db 1410 CCATCGAGGGCGGTCAAGTCAGGCTACGGCAAGGGAGCGCCCTCTCAAGTGAACCG 1469  
 Qy 1526 ACAAGTCAGATCGAGTCTGGCTCCGACCCACCTACACCTCTAGGGCACCATCG 1585  
 Db 1470 GCACGCCACAACT-----CAGATCTGGGTTCCGATGA 1505  
 Qy 1586 TCCCGGCCAGGGCTCCTCGCGTGGCGCGCTGCAAGGTCATTGACGACCAAGGGCAA 1645  
 Db 1506 GTGCCACCCCTCTCCGAGCTGGCTGGTNAAGGGGGGGGGGGGACCGGACCA 1565  
 Qy 1646 TCGAAAGTGTGCTGCTGCCCTGCCAAGGAGACGACGGCATCTGGCGSGCCCTTA 1705  
 Db 1566 TCGCGAGGGCGGTGGAGTCGCGCGGGAGGCCCTACGGGGFCCTCTCGC 1617  
 Qy 1706 AGCCGACTTGGAGGACGGAGGGCGCGAGCGCGCGCGCGCGCGCG 1765  
 Db 1618 -CTACGACGAGGCCAGGAGCGAGGGCGCTGACCGCTCCGACCTGCTGCGGGTAGCGAG 1676  
 Qy 1766 ACCAGCTCATGCCGAGGTGGCGCGGAGCCAAACACCGCTCTGTCATGGAGACGG 1825  
 Db 1677 ACAAGTGTGACTCGGTTGGGGAGCACCCAAACCAACAGATCTGTCCTCAACACGG 1736  
 Qy 1826 GCACCCCGAGAGTGGCCCTGGCTGACGCCACGCCCGCGCTACAGGCGCTGGAG 1885  
 Db 1737 GTCTCGTGGCTGTGTCCTGGCTTCCAGACCCGGGGCTGGTACCTGTTAC 1796  
 Qy 1886 GGGCACGACGACGCGCAATCCATGGCCACGCTGTCTGGGACTACACCCCTCG 1945  
 Db 1797 CGGGCACGGCGCGCGAGGACCGCCACGCCCGCGCTCTAGGTGACGTCACCGAGG 1856  
 Qy 1946 GCAAGCTGCTCTGACTCTGCC-----AAGCCCTGGAGACACCCCGGTTC 1996  
 Db 1857 GCAAGCTCACCGAGCTCTGGCGCGCCAGAACCGAGCGCTCGGGCCACCCCA 1916  
 Qy 1997 TCAACTCCGACGGAGCTGGGAGCTGGAGGAGCTAGTGGCTGGTGGAGGATA 2056  
 Db 1917 CGACGTCACCCGGCGTCGACACCGAGCGACTGCTGGGGCTGCGTGGTAC 1976  
 Qy 2057 GTTACGAGTTGGCTGAGGAGCTCAATTGCGCTGGGACGCTAGTGGCTGGTACA 2116  
 Db 1977 GCTGGTTCGACAGGAGACGTCAGGGCTGGTGGGAGCTGGCTGGTACA 2036  
 Qy 2117 CCACTTGGCTTCAACTCTCGCTGTCAGAACGGC---GGCAAGCTGAGGCT 2173  
 Db 2037 CCTCGTCAAGACGCGCCCGACGCTGGCTGACGTCACGGTGTGAGGTC 2096  
 Qy 2174 CCCTCTCGTGAAGACACCGGCTCGTACGGGCGCACAGTGGCCACACTACGTC 2233







STREET: 4365 Executive Drive, Suite 1600  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Disquette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FastSee for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/134.078  
 FILING DATE: 13-AUG-1998  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/949,026  
 FILING DATE: 10-OCT-1997  
 APPLICATION NUMBER: 60/056,916

FILING DATE: 06-DEC-1996  
 ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.  
 REGISTRATION NUMBER: 38,347  
 REFERENCE/DOCKET NUMBER: 0910/024002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858/677-1456  
 TELEFAX: 858/677-1465

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2166 base pairs  
 TYPE: nucleic acid  
 STRANGENESS: double  
 TOPOLOGY: linear  
 FEATURE:

NAME/KEY: Coding Sequence  
 LOCATION: 1...2163

US-09-134-078-5

Query Match 5.4%; Score 135.8; DB 4; Length 2166;  
 Best Local Similarity 53.5%; Pred. No. 1.6e-20; Mismatches 247; Indels 0; Gaps 0;

Matches 284; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

Qy 207 GCTCGGTTCACATTCACCAAACTCTGTCGAGAGAGCAGGAGATGGCAAAAGA 266  
 Db 258 GCTCGGTCTACCTCTGAAACAGAGACCTCTGGAGAAGGGCATGGAGAAGA 317  
 Qy 267 GGCCATCGCTAAAGAGTGCATCTGATCTGGCCGACTATCACATCAGCTCCC 326  
 Db 318 AGTTAGGAAATCGGTTGATGAGCTCTGACATGACATTCACAGAAACCC 377  
 Qy 327 TCTCGGTGGAGCTGGCTCGAGGATGGTGGAGGATCGTTCTGGGGCTGGAGC 386  
 Db 378 TCTTGTGGAGGATGGAGTACTACTCGAGAGATCTGCTGTTCTGGAAATGGC 437  
 Qy 387 TCGGGTCTCATCCGGCATCGAGACTGGAGTGGAGCTGGCATAAACGACTTGT 446  
 Db 438 TTACGCTTGTCAAGGGACTTCACTCAAGGGTGGCATAAACGACTTGT 497  
 Qy 447 GTGCAATGATCAAGAGGAAGGGCATGATGGTGCAGGACATGTCAGGGGGCCT 506  
 Db 498 CGGGACACACCAAGAACGACAGCATGGTAGTGGACAGATGTCGAGGAGCCT 557  
 Qy 507 CGCGAAATCTCGCACTCCGTTCCAGATGGTGTGGAGAGCTCCCGGGTGCCT 566  
 Db 558 CAGAAATATCTGAAAGGTTTGATGCTCAAGAAGCAACCCGGACGCT 617  
 Qy 567 CAGAGGGCTACATGGCATGGCTGCTGGAGAACCTATCTGAA 626  
 Db 618 GATGAGGCTTACACAAACTGATGGAAATACTGTCACAGAACGATGGTTGAA 677  
 Qy 627 TGGATGCTTCAGGAAGGAATGGGTTGGATGCTCAATCATAGCGACTGGAC 686  
 Db 678 GAGGTTCTCAGGGAGAATGGGATTCGGCTTCGATAGCGACTGGTACCGGG 737

RESULT 7  
 US-09-103-840A-2  
 ; Sequence 2, Application US/09103840A  
 ; Patent No. 6294328  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLEISCHMAN, Robert D.  
 ; APPLICANT: WHITE, Owen R.  
 ; APPLICANT: FRAZER, Claire M.  
 ; APPLICANT: VENNER, John C.  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
 ; FILE REFERENCE: 24166-2007.00  
 ; CURRENT APPLICATION NUMBER: US/09/103,840A  
 ; CURRENT FILING DATE: 1998-06-24  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 4403765  
 ; TYPE: DNA  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; FEATURE:  
 ; OTHER INFORMATION: CDC 151  
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
 ; OTHER INFORMATION: represent a, t, c or g  
 US-09-103-840A-2

Query Match 4.5%; Score 111.6; DB 4; Length 4403765;  
 Best Local Similarity 52.0%; Pred. No. 1.6e-14; Mismatches 289; Indels 30; Gaps 3;

Matches 345; Conservative 0; Mismatches 289; Indels 30; Gaps 3;

Qy 1723 GAGGGCAGCAGCGGGAGCATGAAAGCTCCGGGTGCGTGACATGGCAC 1782  
 Db 217690 GAGGGCTTGTGACAGCGCGCATGTCGTCGCCATGGGTCAAGATGCCGA 217749  
 Qy 1783 GTCGCCGCCGACCCAAACACCGTGTGTCATGGAGACGGGACCCGGAGGATG 1842  
 Db 217750 GTCGGGTGCGCCACCGGAGATACCGTGTGGTGTGAGAGGGACCCGGTACCATG 217809  
 Qy 1843 CCCGGGCGACCCACCCCCGGCTGATCCAGGCCCTGGTACGGCGCAAGAGGGC 1902  
 Db 217810 CCTTGGGGACTCGGTGAAACCCATCATGGAGCCCTGGTATCCGGCCAGGGTGGC 217869  
 Qy 1903 AACCTGATGGCGACGCTGTGCTTGCGACTACAAACCCCTGGCGACGCTGTCAGC 1962  
 Db 217870 CAGGCCGTTGCGGAGATGTTGACCGGGAGGTGAATCCTCGGGGGCTGCCGATCACC 217929  
 Qy 1953 TTCCCCAGGGCTGCGAGGACACCCGGTTCTCACTTCGACGACGGAGCCGGCG 2021  
 Db 217930 TCCCCGTTGATCTGGTACGGCCACGCTGCAACGCCGAGCTGGTCCCGTG 217989  
 Qy 2022 -----CAGCTGTACGGGGAGGAGCTACGGGGTACAGSTACTACGAG 2067  
 Db 217950 GGGACATCGGACACGATCCACTACCGAGGGCGCGATGTGGTACCCGGTGGC 218049  
 Qy 2068 TTTGGCGGAAGGAGCGTCAATTCGGCTTGGCGACCGCGCTGCTCACACCACTTGGC 2127  
 Db 218050 AGCACAAATCTGACCCGATGTTGCGTTGCGTCAAGGCTTACCGATTGCG 218109  
 Qy 2128 TTTCGATCTCTGGTCTGTCACAGGAGCGCAAGCTGAGCGTGTGGTCCCTGCGAAG 2187  
 Db 218110 TATGTTGACTCTGGTGGAGCGGC--GGCCACACCGTGCAGCCAGTTCAGCCTTAC 218166  
 Qy 2188 AACACCGCTCTGGCGCCACAGGGGCCAGCTACGTCAGCCCTCCAGGCG 2247  
 Db 218167 AACACGGGACGCGACGGGGCTGGCGACGACTGGTACCCGGC 218226  
 Qy 2248 GCGAAGATTAAACGCCCGTCAGGAGCTCAAGGGCTTCGCAAAGGGCTGCAACTGCAGCCC 2307



RESULT 10  
US-09-147-236-10  
Sequence 10, Application US/09147236A  
; Patent No. 6316251  
; GENERAL INFORMATION:  
; APPLICANT: TONOUCHI, Naoto  
; APPLICANT: TSUCHIDA, Takayasu  
; APPLICANT: YOSHIMURA, Fumihiro  
; APPLICANT: YAHARA, Naoki  
; APPLICANT: HAYASHI, Takahisa  
; TITLE OF INVENTION: NOVEL GENES, AND NOVEL BETA-GLUCOSIDASE  
; FILE REFERENCE: 6537-011-0PCT  
; CURRENT APPLICATION NUMBER: US/09/147,236A  
; CURRENT FILING DATE: 1999-04-08  
; EARLIER APPLICATION NUMBER: PCT/JP97/03633  
; EARLIER FILING DATE: 1997-10-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 16836  
TYPE: DNA  
ORGANISM: Acetobacter xylinum  
FEATURE: CDS  
NAME/KEY: CDS  
LOCATION: (1891)..(2922)  
FEATURE:  
; OTHER INFORMATION: Nucleotide sequence is the same as SEQ ID NO:1  
FEATURE:  
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, c, or  
; OTHER INFORMATION: t  
US-09-147-236-10

Query Match 4.1%; score 101.4; DB 4; Length 16836;  
Best Local Similarity 50.5%; Pred. No. 6.6e-13; Matches 246; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

QY 422 TGCAGGCTACGACGAAAGGACTTTTGCAATGATCAGGAGCAGGGCATGGTGC 481  
Db 13025 TGTATCCTCCACGCTCAAGCTATTCGATGATGACCTGGCATGACATGACATGAGA 13084

QY 482 AGAGCATCGTCACGGAGGGCTCCCTGGAATCTAGGACTCCCGTCCAGATGCTG 541  
Db 13085 GCGGGATATGACCTCTGGCTGAGATCGCTGAAAGCAGCTGGCAGTCAGATCGCG 13144

QY 542 TGCAGGACTCCACGGGGCTCCCTGGAATCTAGGACTCCCGTCCAGATGCTG 601  
Db 13145 TTGAAACCGGCATCCGGCGCGCTCATGCGCTACACCGGTACAGACTGTATG 13204

QY 602 GCAGCAGGACCTTAATATCTGTGGATGGCTGAAAGGATGGGGTGGATGCC 661  
Db 13205 CGTGTGAAACCCGTACCTGACAGAGCTGGCATATCCGGCT 13264

QY 662 TAATCATGAGCGACTGGTACGGACATACGTTACAGAACGGCTTGCGGGCTCG 721  
Db 13265 TTGTCATGTCGCACTGGGGGCCACGCACTCCCGCGGGCGCTGGGGCTGG 13324

QY 722 ACCTCGA 728  
Db 13325 ATCGAGA 13331

RESULT 11  
US-08-387-942C-1  
Sequence 1, Application US/08387942C  
; Patent No. 5939589  
; GENERAL INFORMATION:  
; APPLICANT: EFTESVAG, HELGA  
; APPLICANT: VALLA, SVEIN  
; APPLICANT: SKJAK-BRAEK, GUDMUND  
; APPLICANT: LARSEN, BIRORN  
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES  
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE  
; NUMBER OF SEQUENCES: 52  
; CURRENT APPLICATION DATA:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
; STREET: P.O.BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387, 942C  
; FILING DATE: 09-MAY-1995  
; CLASIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1809-106P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-205-8000  
; TELEFAX: 703-205-0500  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12588 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Azotobacter vinelandii  
; STRAIN: E

QY 362 ATCCGTTCTGGGGCTTGGAGCTGCGGCTCATCCGGCACTGGAG 421  
Db 12905 GGGTGGGACCTGACCGGGGCACTTGAATATGGCGAAG 12964

QY 362 ATCCGTTCTGGGGCTTGGAGCTGCGGCTCATCCGGCACTGGAG 421

Db 12965 ATCCGTTGAGACCCGGCGCATGGCAGCACCATGGGGGTCAGTCAGCATG 13024  
QY 422 TCCAGGCTACGATCAAGCAGCTTTTGCAATGATCAGGAGCAGGGCATGGTGC 481  
Db 13025 TGTATCCTCCACGCTCAAGCTATTCGATGATGACCTGGCATGACATGAGA 13084

QY 482 AGAGCATCGTCACGGAGGGCTCCCTGGAATCTAGGACTCCCGTCCAGATGCTG 541  
Db 13085 GCGGGATATGACCTCTGGCTGAGATCGCTGAAAGCAGCTGGCAGTCAGATCGCG 13144

QY 542 TGCAGGACTCCACGGGGCTCCCTGGAATCTAGGACTCCCGTCCAGATGCTG 601  
Db 13145 TTGAAACCGGCATCCGGCGCGCTCATGCGCTACACCGGTACAGACTGTATG 13204

QY 602 GCAGCAGGACCTTAATATCTGTGGATGGCTGAAAGGATGGGGTGGATGCC 661  
Db 13205 CGTGTGAAACCCGTACCTGACAGAGCTGGCATATCCGGCT 13264

QY 662 TAATCATGAGCGACTGGTACGGACATACGTTACAGAACGGCTTGCGGGCTCG 721  
Db 13265 TTGTCATGTCGCACTGGGGGCCACGCACTCCCGCGGGCGCTGGGGCTGG 13324

QY 722 ACCTCGA 728  
Db 13325 ATCGAGA 13331





PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/625,140  
 FILING DATE: 10-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dillahunty, T. Gene  
 REGISTRATION NUMBER: 25,423  
 REFERENCE/DOCKET NUMBER: 010055-056  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-854-7400  
 TELEFAX: 415-854-8275  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 MOLECULE TYPE: DNA (genomic)  
 LENGTH: 3033 base pairs  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Trichoderma reesei  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: Join(311..375, 446..2205, 2270..2679)  
 FEATURE:  
 NAME/KEY: intron  
 LOCATION: 376..445  
 FEATURE:  
 NAME/KEY: intron  
 LOCATION: 2206..2269  
 US-08-462-090-1  
 Query Match 3.3%; Score 83.8; DB 3; Length 3033;  
 Best Local Similarity 50.1%; Pred. No. 2.7e-09; Matches 264; Conservative 0; Mismatches 257; Indels 6; Gaps 2;  
 Matches 264; Conservative 0; Mismatches 257; Indels 6; Gaps 2;  
 QY 214 TCCACATTCACAAACATCTGTCGAAGAGGAGATGGCAAGAGGCCATC 273  
 Db 720 TGCAGCTGGATGTCATTGTTCGGCGAACGGAGCTTCATCGGTGAGGAGTGAAG 779  
 QY 274 GCTAAGATGTCGCGATGATGATCTCGGCC--GACTATCACACATCACACCTCCCTCTC 330  
 Db 780 GCTCGGGATTCATGTCATACGGCTGGCTGGCGCTGGAAAGACTCGCG 839  
 QY 331 GGTGACCGTGGTTGAGTCGTTGGGAGATCCCTCGGCCGCTTGGAGCTGCG 390  
 Db 840 GCGGTGCGAACCTGGGGCTCGGGTCAATCATTCACCGGATTCATGGT 899  
 QY 391 GCTCTCATCGCGCATCAGACACTGGAGGAGCAGCTGGCGCTAGATCAGCACTTGTG 450  
 Db 900 CAAACCATCAAGCGCATCCAGCAGCGGCTTGGCTGCAGCGAGCGAGAC 959  
 QY 451 ATGATCAGGAGACAGCGGATGAGGTGGCTGAGASCATCGTCACGAGCGGGCTTCGT 510  
 Db 960 AACGAGCAGGAGCTCAATCGAGAACCATTCAGGACACAGATGACCGACATCCAT 1019  
 QY 511 GAAATCPACGCCCTCCGTCAGATGCTGCGAGACTCCAGCCGGGTGGCTCATG 570  
 Db 1020 GAGCTGATACATGGCATTGCGACGGCTTGGATGGCTATGAGCTGGCTCATG 1076  
 QY 571 AGCGGACAGCATCAATCGCGTCTCGAGGAGAACCCATAATCTCTGAGTCATGG 630  
 Db 1077 TSCCTCGPACACAGGCAATCCATCCACCTGGCCCTGGAGGATCAGTACACCTGAGACT 1136  
 QY 631 ATGCTTGAAAGGAAGGATGGGTTGGATGGCTTAATCATGAGCGACTGGTGGACATAC 690  
 Db 1137 GCTCTGAAAGACAGCTGGGTTCCAGGCTATGATCATGAGCGACTGGACAC 1196  
 QY 691 AGTACCCAGAGGCCGTTGCGAGGCTCGACCTCGAGATGCCCG 737  
 Db 1197 AGCAGTCACAAAGCGCGAATTCTGGCTTGACATGCAATGCTGG 1243  
 US-08-462-090-1  
 Query Match 3.3%; Score 83.8; DB 3; Length 3033;  
 Best Local Similarity 50.1%; Pred. No. 2.7e-09; Matches 264; Conservative 0; Mismatches 257; Indels 6; Gaps 2;  
 Matches 264; Conservative 0; Mismatches 257; Indels 6; Gaps 2;  
 QY 214 TCCACATTCACAAACATCTGTCGAAGAGGAGATGGCAAGAGGCCATC 273  
 Db 720 TCGAGCTGGATGTCATTGTTCATCGCGAACGGAGCTTCATCGGTGAGGAGTGAAG 779  
 QY 274 GCTAAGATGTCGCGATGATGATCTCGGCC--GACTATCACACATCACACCTCCCTCTC 330  
 Db 780 GCTCTCATCGCGCATCAGACACTGGAGGAGCAGCTGGCGCTGGAAAGACTCGCG 839  
 QY 331 GGTGACCGTGGTTGAGTCGTTGGGAGATCCCTCGGCCGCTTGGAGCTGCG 390  
 Db 840 GCGGTGCGAACCTGGGGCTCGGGTCAATCATTCACCGGACATTCACGGGCAATGGT 899

QY 391 GCTCTCATCCGGCGCATTCAGACGACACTGGAGCAGCTAGATCAGACATTGTC 450  
 Db 900 CAACCATCAACGGCATCCAGTGGTAGCGCAGCGACAGCGAACACTATATCCTC 959  
 QY 451 AATGATCAGGAGGACAGCGCATGATGTCAGAGCATGTCACGGAGGCGCTCTCGT 510  
 Db 960 AACGAGCAGGAGCTCAATGAGAAACCATTCAGAGCACCCAGATACCGAATCTCCAT 1019  
 QY 511 GAATCTACGCACTCCCGTCCAGATGCTGCGAGACTCCAGCGGGTGGTTCATG 570  
 Db 1020 GACCTGTATACTTGGCCATTGCGACCGGGTC--AGGCCAATGTCGCTCTGTCATG 1076  
 QY 571 ACGCGTCAATGCAATAGCGTGTGCGTGGCGAGAACCTAAATATCTGATGG 630  
 Db 1077 TGTCTGTACACAGGTCAATACACCTGGCGTGCAGGATCAGTACACCGCTGCAGACT 1136  
 QY 631 ATGCTTCAAAGGAATGGGTGGATGGCTATCATGAGGGACTGACCGCACATAC 690  
 Db 1137 GTCTGAAAGACCAAGCTGGGTTCCAGGTATGTCATGAGGACTGGAACGCCAC 1196  
 QY 691 AGTACCAAGAGGGTGGAGGGCTCGACCTCGAGATCCCCG 737  
 Db 1197 ACCACTGCTCAAAGGCGAATTCTGGCTTGACATGTCATGCTGG 1243

Search completed: May 3, 2003, 23:04:10  
 Job time : 3077.09 secs

